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Citation style: Idziak Dominika, Hasterok Robert, Betekhtin Alexander, Borowska-Żuchowska Natalia, Chwiałkowska Karolina, Kwaśniewska Jolanta, Kwaśniewski Mirosław, Robaszkiewicz Ewa, Siwińska Dorota, Wolny Elżbieta, Chromiński Kornel, Tkacz Magdalena. (2015). Brachypodium distachyon - a model plant to study grass genome structure, dynamics and evolution. "Biotechnologia" (T. 96, nr 1 (2015), s. 43), doi 10.5114/bta.2015.54184



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***Brachypodium distachyon* – a model plant to study grass genome structure, dynamics and evolution**

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Ecologically, as well as economically, Grasses (Poaceae) belong to the most important groups of plants. Members of the Poaceae, such as wheat, rice, and maize, provide a vast majority of human food worldwide and dominate the vegetation in various habitats across all continents and climate zones. However, the experimental and genomic tractability of most grass crops is frequently hindered by their large genome sizes and polyploidy. *Brachypodium distachyon*, a small annual weedy grass, emerged several years ago as a model system to study various aspects of genome organisation, functioning, and evolution in temperate cereals and grasses. *B. distachyon* possesses numerous attributes sought after in a model organism. These include a favourable phylogenetic position within the 'core' Poaceae species, a small (~350 Mb) genome, small physical stature, self-fertility, a short life cycle and undemanding growth requirements. It also has an ever growing repertoire of experimental resources such as germplasm collections, complete and almost fully-annotated genome sequence, large-insert genomic DNA libraries, expressed sequence tag (EST) databases, as well as efficient *Agrobacterium*-mediated transformation protocols and availability of mutant collections. The recent years have shown that *B. distachyon* can serve as an excellent model system to study cell wall composition and development, biomass accumulation, plant-pathogen interactions and reaction to abiotic stress. Due to the compactness of its genome and low basic chromosome number, it also provides unique opportunities to address many novel and important areas of plant molecular cytogenetics.

Advanced cytomolecular techniques, such as fluorescence in situ hybridisation (FISH) with evermore sophisticated probes coupled with state-of-the-art microscopy and digital image acquisition offer an unprecedented insight into various aspects of nuclear genome organisation and dynamics. One of the most informative cytomolecular tools is chromosome painting (CP), which enables unique and unambiguous visualization of individual chromosomes or large segments not only during cell division but also during the interphase. It can also be employed to study the karyotype evolution among closely related species and the phylogenetic relationship at the level of the chromosome. Another powerful cytomolecular technique utilises the application of specific antibodies linked with fluorochromes. Such antibodies allow selective localisation of epigenetically modified components of chromatin, such as methylated DNA and histones. They may also target various proteins that compose specific biological structures, like the synaptonemal complex, or are responsible for various enzymatic processes, for example recombination events during meiosis in plants.

This presentation summarises the present status of analyses of plant genome structure, dynamics and evolution using *B. distachyon* and some of its relatives. The on going research projects address various important scientific problems such as elucidating the mechanisms responsible for the grass karyotype evolution and divergence, deciphering the factors that determine the distribution of individual chromosomes within an interphase nucleus, or the chromosomal behaviour during meiotic cell division. Other on going investigations attempt to answer the questions whether there are hot spots of structural rearrangement in *Brachypodium* chromosomes and which epigenetic processes play a crucial role in *B. distachyon* embryo development and selective silencing of rRNA genes in *Brachypodium* allopolyploids.

Acknowledgments

The authors acknowledge financial support from the Polish National Science Centre (grants no. 2012/04/A/NZ3/00572 and 2014/14/M/NZ2/00519).